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RAW SEQUENCE LISTING

DATE: 03/01/2002

PATENT APPLICATION: US/09/870,759

TIME: 15:00:28

Input Set : A:\terman.txt

Output Set: N:\CRF3\03012002\I870759.raw

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3 <110> APPLICANT: Terman, David S
5 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
7 <130> FILE REFERENCE: 870759
9 <140> CURRENT APPLICATION NUMBER: US 09/870,759
C--> 10 <141> CURRENT FILING DATE: 2002-01-14
12 <150> PRIOR APPLICATION NUMBER: US 60/208,128
13 <151> PRIOR FILING DATE: 2000-05-30
15 <160> NUMBER OF SEQ ID NOS: 166
17 <170> SOFTWARE: PatentIn version 3.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 801
21 <212> TYPE: DNA
22 <213> ORGANISM: Staphylococcus sp.
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27 tctacaccca acgttttagc agagagtcaa ccagatccta aaccagatga gttgcacaaa      120
29 tcgagtaaat tcactgggtt gatggaaaat atgaaagttt tgtatgatga taatcatgta      180
31 tcagcaataa acgttaaadc tatagatcaa tttctatact ttgacttaat atattctatt      240
33 aaggacacta agttagggaa ttatgataat gttcgagtcg aatttaaaaa caaagattta      300
35 gctgataaat acaaagataa atacgtagat gtgtttggag ctaattatta ttatcaatgt      360
37 tatttttcta aaaaaacgaa tgatattaat tcgcatcaaa ctgacaaaacg aaaaacttgt      420
39 atgtatggtg gtgtaactga gcataatgga aaccaattag ataaatatag aagtattact      480
41 gttcgggtat ttgaagatgg taaaaattta ttatcttttg acgtacaaac taataagaaa      540
43 aaggtgactg ctcaagaatt agattaccta actcgtcact atttggtgaa aaataaaaaa      600
45 ctctatgaat ttaacaactc gccttatgaa acgggatata ttaaatatat agaaaatgag      660
47 aatagctttt ggtatgacat gatgcctgca ccaggagata aatttgacca atctaaatat      720
49 ttaatgatgt acaatgacaa taaaatggtt gattctaaag atgtgaagat tgaagtttat      780
51 cttacgacaa agaaaaagtg a                                     801
54 <210> SEQ ID NO: 2
55 <211> LENGTH: 886
56 <212> TYPE: DNA
57 <213> ORGANISM: Artificial Sequence
59 <220> FEATURE:
60 <223> OTHER INFORMATION: Synthetic Sequence
62 <400> SEQUENCE: 2
63 cggctcacag cgcgcccggc tattctcgca ggatcagtcg acatgtataa gagattattt      60
65 atttcacatg taattttgat attcgcactg atattagtta tttctacacc caacgtttta      120
67 gcagagagtc aaccagatcc taaaccagat gaggtcaca aatcgagtaa attcactggt      180
69 ttgatggaaa atatgaaagt tttgtatgat gataatcatg tatcagcaat aaacgttaaa      240
71 tctatagatc aatttctata ctttgactta atatattcta ttaaggacac taagttaggg      300
73 aattatgata atgttcgagt cgaatttaaa aacaaaagatt tagctgataa atacaaaagat      360
75 aaatacgtag atgtgttttg agctaattat tattatcaat gttatttttc taaaaaacg      420
77 aatgatatta attcgcacaa aactgacaaa cgaaaaactt gtatgtatgg tgggtgtaact      480

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79 gagcataatg gaaaccaatt agataaatat agaagtatta ctgttcgggt atttgaagat      540
81 ggtaaaaaatt tattatcttt tgacgtacaa actaataaga aaaaggtgac tgctcaagaa      600
83 ttagattacc taactcgtca ctatttggtg aaaaataaaa aactctatga atttaacaa      660
85 tggccttatg aaacgggata tattaatttt atagaaaatg agaatagctt ttggatgac      720
87 atgatgcctg caccaggaga taaatttgac caatctaaat atttaatgat gtacaatgac      780
89 aataaaaatg ttgattctaa agatgtgaag attgaagttt atcttaacgac aaagaaaaag      840
91 tgaggatcca gacatgataa gataccttga tgagtttggg caaacc                      886
94 <210> SEQ ID NO: 3
95 <211> LENGTH: 24
96 <212> TYPE: DNA
97 <213> ORGANISM: Unknown
99 <220> FEATURE:
100 <223> OTHER INFORMATION: Primer
102 <400> SEQUENCE: 3
103 ggcgtcgaca tgtataagag atta                                          24
106 <210> SEQ ID NO: 4
107 <211> LENGTH: 24
108 <212> TYPE: DNA
109 <213> ORGANISM: Unknown
111 <220> FEATURE:
112 <223> OTHER INFORMATION: Primer
114 <400> SEQUENCE: 4
115 gccggtacct cactttttct ttgt                                          24
118 <210> SEQ ID NO: 5
119 <211> LENGTH: 22
120 <212> TYPE: DNA
121 <213> ORGANISM: Unknown
123 <220> FEATURE:
124 <223> OTHER INFORMATION: Primer
126 <400> SEQUENCE: 5
127 tatgaaagtt ttgtatgatg at                                          22
130 <210> SEQ ID NO: 6
131 <211> LENGTH: 20
132 <212> TYPE: DNA
133 <213> ORGANISM: Unknown
135 <220> FEATURE:
136 <223> OTHER INFORMATION: Primer
138 <400> SEQUENCE: 6
139 agtgacgagt taggtaatct                                          20
142 <210> SEQ ID NO: 7
143 <211> LENGTH: 1443
144 <212> TYPE: DNA
145 <213> ORGANISM: Staphylococcus aureus
147 <220> FEATURE:
148 <221> NAME/KEY: CDS
149 <222> LOCATION: (262)..(1032)
150 <223> OTHER INFORMATION:
153 <400> SEQUENCE: 7
154 ccaaaaataat ggcaagtact ccgttgtcaa taccaagtaa gtaagatatc tgaaatgtat      60

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156	aatagagtaa	aaatgaaatc	tttttattat	attatagaca	agtataaaaa	aggtatagta	120
158	atatatgtat	gtataagtaa	ataatgataa	ttctataatt	attgtatata	actaataatt	180
160	acttcgacaa	aaataatcta	ttatccaaat	atttttagata	ataaaaaagtt	tgtatggaat	240
162	tatgcttttag	agggtgagcaa	a atg	aaa aaa aca	gca ttt ata	cta ctt tta	291
163			Met	Lys Lys Thr	Ala Phe Ile	Leu Leu Leu	
164			1		5	10	
166	ttc att gcc	cta acg tgg	aca aca	agt cca ctt	gta aat ggt	agc gag	339
167	Phe Ile Ala	Leu Thr Trp	Thr Thr	Ser Pro	Leu Val Asn	Gly Ser Glu	
168		15		20		25	
170	aaa agc gaa	gaa ata aat	gaa aaa	gat ttg cga	aaa aag tct	gaa ttg	387
171	Lys Ser Glu	Glu Ile Asn	Glu Lys	Asp Leu Arg	Lys Lys Ser	Glu Leu	
172		30		35		40	
174	cag gga gca	gct tta ggc	aat ctt	aaa caa atc	tat tat tac	aat gaa	435
175	Gln Gly Ala	Ala Leu Gly	Asn Leu	Lys Gln Ile	Tyr Tyr Tyr	Asn Glu	
176		45		50		55	
178	aaa gct aaa	act gaa aat	aaa gag	agt cac gat	caa ttt tta	cag cat	483
179	Lys Ala Lys	Thr Glu Asn	Lys Glu	Ser His Asp	Gln Phe Leu	Gln His	
180		60		65		70	
182	act ata ttg	ttt aaa ggc	ttt ttt	aca aat cat	tca tgg tat	aac gat	531
183	Thr Ile Leu	Phe Lys Gly	Phe Phe	Thr Asn His	Ser Trp Tyr	Asn Asp	
184	75		80		85	90	
186	tta tta gta	gat ttt gat	tca aag	gat att gtt	gat aaa tat	aaa ggg	579
187	Leu Leu Val	Asp Phe Asp	Ser Lys	Asp Ile Val	Asp Lys Tyr	Lys Gly	
188		95		100		105	
190	aaa aaa gta	gac tta tat	ggg gct	tat tat ggt	tat caa tgt	gcg ggt	627
191	Lys Lys Val	Asp Leu Tyr	Gly Ala	Tyr Tyr Gly	Tyr Gln Cys	Ala Gly	
192		110		115		120	
194	ggg aca cca	aac aaa aca	gct tgc	atg tat ggt	ggg gta acg	tta cat	675
195	Gly Thr Pro	Asn Lys Thr	Ala Cys	Met Tyr Gly	Gly Val Thr	Leu His	
196		125		130		135	
198	gat aat aat	cga ttg acc	gaa gag	aaa aaa gtg	ccg atc aat	tta tgg	723
199	Asp Asn Asn	Arg Leu Thr	Glu Glu	Lys Lys Val	Pro Ile Asn	Leu Trp	
200		140		145		150	
202	cta gac ggt	aaa caa aat	aca gta	cct ttg gaa	acg gtt aaa	acg aat	771
203	Leu Asp Gly	Lys Gln Asn	Thr Val	Pro Leu Glu	Thr Val Lys	Thr Asn	
204	155		160		165	170	
206	aag aaa aat	gta act gtt	cag gag	ttg gat ctt	caa gca aga	cgt tat	819
207	Lys Lys Asn	Val Thr Val	Gln Glu	Leu Asp Leu	Gln Ala Arg	Arg Tyr	
208		175		180		185	
210	tta cag gaa	aaa tat aat	tta tat	aac tct gat	gtt ttt gat	ggg aag	867
211	Leu Gln Glu	Lys Tyr Asn	Leu Tyr	Asn Ser Asp	Val Phe Asp	Gly Lys	
212		190		195		200	
214	gtt cag agg	gga tta atc	gtg ttt	cat act tct	aca gaa cct	tcg gtt	915
215	Val Gln Arg	Gly Leu Ile	Val Phe	His Thr Ser	Thr Glu Pro	Ser Val	
216		205		210		215	
218	aat tac gat	tta ttt ggt	gct caa	gga cag aat	tca aat aca	cta tta	963
219	Asn Tyr Asp	Leu Phe Gly	Ala Gln	Gly Gln Asn	Ser Asn Thr	Leu Leu	
220		220		225		230	
222	aga ata tat	aga gat aat	aaa acg	att aac tct	gaa aac atg	cat att	1011

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223 Arg Ile Tyr Arg Asp Asn Lys Thr Ile Asn Ser Glu Asn Met His Ile
224 235                240                245                250
226 gat ata tat tta tat aca agt taaacatggt agttttgaac acgtaatggt      1062
227 Asp Ile Tyr Leu Tyr Thr Ser
228                255
230 cagattatta tgaaccgaga ataacttgaa agttttacaag cagtaaaaaa agtatatgtg      1122
232 ctataatatg ctttgagcaa gttggataga tgggtgctat ctgagtataa ggaggtggtg      1182
234 cctatgggtg cattactgaa atctttagaa aggagacgcc taatgattac aattagtacc      1242
236 aatggtgcag tttggtttat tccttattgc attgataggt ctagtaatca agcttattga      1302
238 attaagcaat aaaaaataac catcgctaac tttggctggt ttcgatgggt aaatgggtat      1362
240 taatttaate tttaatctaa aatagccacc gtcttttttaa cggggtcatt agggtaacat      1422
242 gtttgcgcac gttgcccttt t
245 (210) SEQ ID NO: 8
246 (211) LENGTH: 257
247 (212) TYPE: PRT
248 (213) ORGANISM: Staphylococcus aureus
250 (400) SEQUENCE: 8
252 Met Lys Lys Thr Ala Phe Ile Leu Leu Leu Phe Ile Ala Leu Thr Trp
253 1                5                10                15
256 Thr Thr Ser Pro Leu Val Asn Gly Ser Glu Lys Ser Glu Glu Ile Asn
257                20                25                30
260 Glu Lys Asp Leu Arg Lys Lys Ser Glu Leu Gln Gly Ala Ala Leu Gly
261                35                40                45
264 Asn Leu Lys Gln Ile Tyr Tyr Tyr Asn Glu Lys Ala Lys Thr Glu Asn
265                50                55                60
268 Lys Glu Ser His Asp Gln Phe Leu Gln His Thr Ile Leu Phe Lys Gly
269 65                70                75                80
272 Phe Phe Thr Asn His Ser Trp Tyr Asn Asp Leu Leu Val Asp Phe Asp
273                85                90                95
276 Ser Lys Asp Ile Val Asp Lys Tyr Lys Gly Lys Lys Val Asp Leu Tyr
277                100               105               110
280 Gly Ala Tyr Tyr Gly Tyr Gln Cys Ala Gly Gly Thr Pro Asn Lys Thr
281                115               120               125
284 Ala Cys Met Tyr Gly Gly Val Thr Leu His Asp Asn Asn Arg Leu Thr
285                130               135               140
288 Glu Glu Lys Lys Val Pro Ile Asn Leu Trp Leu Asp Gly Lys Gln Asn
289 145               150               155               160
292 Thr Val Pro Leu Glu Thr Val Lys Thr Asn Lys Lys Asn Val Thr Val
293                165               170               175
296 Gln Glu Leu Asp Leu Gln Ala Arg Arg Tyr Leu Gln Glu Lys Tyr Asn
297                180               185               190
300 Leu Tyr Asn Ser Asp Val Phe Asp Gly Lys Val Gln Arg Gly Leu Ile
301                195               200               205
304 Val Phe His Thr Ser Thr Glu Pro Ser Val Asn Tyr Asp Leu Phe Gly
305                210               215               220
308 Ala Gln Gly Gln Asn Ser Asn Thr Leu Leu Arg Ile Tyr Arg Asp Asn
309 225               230               235               240
312 Lys Thr Ile Asn Ser Glu Asn Met His Ile Asp Ile Tyr Leu Tyr Thr
313                245               250               255

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316 Ser
320 <210> SEQ ID NO: 9
321 <211> LENGTH: 1712
322 <212> TYPE: DNA
323 <213> ORGANISM: Staphylococcus aureus
325 <220> FEATURE:
326 <221> NAME/KEY: CDS
327 <222> LOCATION: (244)..(1044)
328 <223> OTHER INFORMATION:
331 <400> SEQUENCE: 9
332 gaactaggta gaaaaataat tatgagaaaa cactatgttg ttaaagatgt ttctgtatat      60
334 aagtttaggt gatgtatagt tacttaattt taaaagcata acttaattaa tataaataac      120
336 atgagattat taaatataat taagtttctt ttaatgtttt tttaattgaa tatttaagat      180
338 tataacatat atttaaagtg tatctagata ctttttggga atgttggata aaggagataa      240
340 aaa atg tat aag aga tta ttt att tca cat gta att ttg ata ttc gca      288
341 Met Tyr Lys Arg Leu Phe Ile Ser His Val Ile Leu Ile Phe Ala
342 1 5 10 15
344 ctg ata tta gtt att tct aca ccc aac gtt tta gca gag agt caa cca      336
345 Leu Ile Leu Val Ile Ser Thr Pro Asn Val Leu Ala Glu Ser Gln Pro
346 20 25 30
348 gat cct aaa cca gat gag ttg cac aaa tcg agt aaa ttc act ggt ttg      384
349 Asp Pro Lys Pro Asp Glu Leu His Lys Ser Ser Lys Phe Thr Gly Leu
350 35 40 45
352 atg gaa aat atg aaa gtt ttg tat gat gat aat cat gta tca gca ata      432
353 Met Glu Asn Met Lys Val Leu Tyr Asp Asp Asn His Val Ser Ala Ile
354 50 55 60
356 aac gtt aaa tct ata gat caa ttt cta tac ttt gac tta ata tat tct      480
357 Asn Val Lys Ser Ile Asp Gln Phe Leu Tyr Phe Asp Leu Ile Tyr Ser
358 65 70 75
360 att aag gac act aag tta ggg aat tat gat aat gtt cga gtc gaa ttt      528
361 Ile Lys Asp Thr Lys Leu Gly Asn Tyr Asp Asn Val Arg Val Glu Phe
362 80 85 90 95
364 aaa aac aaa gat tta gct gat aaa tac aaa gat aaa tac gta gat gtg      576
365 Lys Asn Lys Asp Leu Ala Asp Lys Tyr Lys Asp Lys Tyr Val Asp Val
366 100 105 110
368 ttt gga gct aat tat tat tat caa tgt tat ttt tct aaa aaa acg aat      624
369 Phe Gly Ala Asn Tyr Tyr Tyr Gln Cys Tyr Phe Ser Lys Lys Thr Asn
370 115 120 125
372 gat att aat tcg cat caa act gac aaa cga aaa act tgt atg tat ggt      672
373 Asp Ile Asn Ser His Gln Thr Asp Lys Arg Lys Thr Cys Met Tyr Gly
374 130 135 140
376 ggt gta act gag cat aat gga aac caa tta gat aaa tat aga agt att      720
377 Gly Val Thr Glu His Asn Gly Asn Gln Leu Asp Lys Tyr Arg Ser Ile
378 145 150 155
380 act gtt cgg gta ttt gaa gat ggt aaa aat tta tta tct ttt gac gta      768
381 Thr Val Arg Val Phe Glu Asp Gly Lys Asn Leu Leu Ser Phe Asp Val
382 160 165 170 175
384 caa act aat aag aaa aag gtg act gct caa gaa tta gat tac cta act      816
385 Gln Thr Asn Lys Lys Lys Val Thr Ala Gln Glu Leu Asp Tyr Leu Thr

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Use of n or xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa

VERIFICATION SUMMARY

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L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:2179 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34

L:3931 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46

L:5010 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53

L:5014 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53

L:5037 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54

L:22523 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:164